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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/041,615

DATE: 02/04/2003 p.6  
TIME: 13:52:26Input Set : A:\cura\_533.us.list.txt  
Output Set: N:\CRF4\02042003\J041615.raw

2 <110> APPLICANT: Casman, Stacie J  
 3 Edinger, Shlomit R  
 4 Ellerman, Karen  
 5 Smithson, Glennda  
 6 Kekuda, Ramesh  
 7 Padigaru, Muralidhara  
 9 <120> TITLE OF INVENTION: Novel GPCR-Like Proteins and Nucleic Acids Encoding Same  
 11 <130> FILE REFERENCE: 21402-233-061  
 13 <140> CURRENT APPLICATION NUMBER: 10/041,615  
 C--> 14 <141> CURRENT FILING DATE: 2003-01-29  
 16 <150> PRIOR APPLICATION NUMBER: 60/259,552  
 17 <151> PRIOR FILING DATE: 2001-01-03  
 19 <150> PRIOR APPLICATION NUMBER: 60/260,544  
 20 <151> PRIOR FILING DATE: 2001-01-09  
 22 <150> PRIOR APPLICATION NUMBER: 60/277,405  
 23 <151> PRIOR FILING DATE: 2001-03-20  
 25 <160> NUMBER OF SEQ ID NOS: 174  
 27 <170> SOFTWARE: CuraSeqList version 0.1  
 29 <210> SEQ ID NO: 1  
 30 <211> LENGTH: 947  
 31 <212> TYPE: DNA  
 32 <213> ORGANISM: Homo sapiens  
 34 <220> FEATURE:  
 35 <221> NAME/KEY: CDS  
 36 <222> LOCATION: (17)..(931)  
 38 <400> SEQUENCE: 1  
 39 tggaaacgaat aactct atg gtg act gaa ttc att ttt ctg ggt ctc tct gat 52  
 40 Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp  
 41 1 5 10  
 43 tct cag gaa ctc cag acc ttc cta ttt atg ttg ttt gta ttc tat 100  
 44 Ser Gln Glu Leu Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr  
 45 15 20 25  
 47 gga gga atc gtg ttt gga aac ctt ctt att gtc ata aca gtg gta tct 148  
 48 Gly Gly Ile Val Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser  
 49 30 35 40  
 51 gac tcc cac ctt cac tct ccc atg tac ttc ctg cta gcc aac ctc tca 196  
 52 Asp Ser His Leu His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser  
 53 45 50 55 60  
 55 ctc att gat ctg tct ctg tca gtc aca gcc ccc aag atg att act 244  
 56 Leu Ile Asp Leu Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr  
 57 65 70 75  
 59 gac ttt ttc agc cag cgc aaa gtc atc tct ttc aag ggc tgc ctt gtt 292  
 60 Asp Phe Phe Ser Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val

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61	80	85	90	
63	cag ata ttt ctc ctt cac ttc ttt ggt ggg agt gag atg gtg atc ctc			340
64	Gln Ile Phe Leu Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu			
65	95	100	105	
67	ata gcc atg ggc ttt gac aga tat ata gca ata tgc aag ccc cta cac			388
68	Ile Ala Met Gly Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His			
69	110	115	120	
71	tac act aca att atg tgt ggc aac gca tgt gtc ggc att atg gct gtc			436
72	Tyr Thr Thr Ile Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val			
73	125	130	135	140
75	aca tgg gga att ggc ttt ctc cat tcg gtg agc cag ttg gcg ttt gcc			484
76	Thr Trp Gly Ile Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala			
77	145	150	155	
79	gtg cac tta ctc ttc tgt ggt ccc aat gag gtc gat agt ttt tat tgt			532
80	Val His Leu Leu Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys			
81	160	165	170	
83	gac ctt cct agg gta atc aaa ctt gcc tgt aca gat acc tac agg cta			580
84	Asp Leu Pro Arg Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu			
85	175	180	185	
87	gat att atg gtc att gct aac agt ggt gtg ctc act gtg tgt tct ttt			628
88	Asp Ile Met Val Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe			
89	190	195	200	
91	gtt ctt cta atc atc tca tac act atc atc cta atg acc atc cag cat			676
92	Val Leu Leu Ile Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His			
93	205	210	215	220
95	cgc cct tta gat aag tcg tcc aaa gct ctg tcc act ttg act gct cac			724
96	Arg Pro Leu Asp Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His			
97	225	230	235	
99	att aca gta gtt ctt ttg ttc ttt gga cca tgt gtc ttt att tat gcc			772
100	Ile Thr Val Val Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala			
101	240	245	250	
103	tgg cca ttc ccc atc aag tca tta gat aaa ttc ctt gct gta ttt tat			820
104	Trp Pro Phe Pro Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr			
105	255	260	265	
107	tct gtg atc acc cct ctc ttg aac cca att ata tac aca ctg agg aac			868
108	Ser Val Ile Thr Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn			
109	270	275	280	
111	aaa gac atg aag acg gca ata aga cag ctg aga aaa tgg gat gca cat			916
112	Lys Asp Met Lys Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His			
113	285	290	295	300
115	tct agt gta aag ttt tagatcttat ataaact			947
116	Ser Ser Val Lys Phe			
117	305			
119	<210> SEQ ID NO: 2			
120	<211> LENGTH: 305			
121	<212> TYPE: PRT			
122	<213> ORGANISM: Homo sapiens			
124	<400> SEQUENCE: 2			
125	Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Glu Leu			

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126 1 5 10 15  
128 Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val  
129 20 25 30  
131 Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu  
132 35 40 45  
134 His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu  
135 50 55 60  
137 Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser  
138 65 70 75 80  
140 Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu  
141 85 90 95  
143 Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly  
144 100 105 110  
146 Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile  
147 115 120 125  
149 Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Thr Trp Gly Ile  
150 130 135 140  
152 Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Leu  
153 145 150 155 160  
155 Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg  
156 165 170 175  
158 Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val  
159 180 185 190  
161 Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile  
162 195 200 205  
164 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp  
165 210 215 220  
167 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val  
168 225 230 235 240  
170 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro  
171 245 250 255  
173 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr  
174 260 265 270  
176 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys  
177 275 280 285  
179 Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys  
180 290 295 300  
182 Phe  
183 305  
185 <210> SEQ ID NO: 3  
186 <211> LENGTH: 948  
187 <212> TYPE: DNA  
188 <213> ORGANISM: Homo sapiens  
190 <220> FEATURE:  
191 <221> NAME/KEY: CDS  
192 <222> LOCATION: (4)..(945)  
194 <400> SEQUENCE: 3  
195 taa atg aga cct aat aac agc att aca gaa ttt gtc ctc ctg gga ttc 48  
196 Met Arg Pro Asn Asn Ser Ile Thr Glu Phe Val Leu Leu Gly Phe

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Input Set : A:\cura\_533\_us\_list.txt  
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197	1	5	10	15	
199	tct cag gat cct ggt atg caa aaa gaa tta ttt gtc atg ttt tta ttc				96
200	Ser Gln Asp Pro Gly Met Gln Lys Glu Leu Phe Val Met Phe Leu Phe				
201	20	25		30	
203	aca tac gtt gtg act gtg ttg ggg aac cag ctc att gtg gtg act atc				144
204	Thr Tyr Val Val Thr Val Leu Gly Asn Gln Leu Ile Val Val Thr Ile				
205	35	40		45	
207	att gcc agc cct tcc ttg ggc tcc cca atg tac ttc ttc ctt gcc tgc				192
208	Ile Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Cys				
209	50	55		60	
211	ctg tca ttt ata gat gct gca tat ttc act gtc att tct ccc aaa ttg				240
212	Leu Ser Phe Ile Asp Ala Ala Tyr Phe Thr Val Ile Ser Pro Lys Leu				
213	65	70		75	
215	att gtg gac tta ctc tgt gat aaa aag act att tcc ttc caa acg ttc				288
216	Ile Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Gln Thr Phe				
217	80	85		90	
219	95				
220	atg ggc caa cta ttt ata gac cac ttc ttt ggt ggt gca gag gcc ttc				336
221	Met Gly Gln Leu Phe Ile Asp His Phe Phe Gly Gly Ala Glu Ala Phe				
222	100	105		110	
223	ctt ctg gtg gtg atg gcc tat gat cgc tat gtt gcc atc tgt aag aca				384
224	Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Thr				
225	115	120		125	
227	ttg cac tat ttg acc atc atg act cga cag gtt tgt atc ctt gca ttg				432
228	Leu His Tyr Leu Thr Ile Met Thr Arg Gln Val Cys Ile Leu Ala Leu				
229	130	135		140	
231	ctg gtg gct gcg aca ggc ggt ttt gtg cat tct gtg ttt caa att gtt				480
232	Leu Val Ala Ala Thr Gly Gly Phe Val His Ser Val Phe Gln Ile Val				
233	145	150		155	
235	gtt gtg tac agt ctc cct ttc tgt ggc gcc aat gtc att gat cat ttc				528
236	Val Val Tyr Ser Leu Pro Phe Cys Gly Ala Asn Val Ile Asp His Phe				
237	160	165		170	
239	175				
240	agt tgt gac atg tat cca tta ttg gaa ctg gca tgt act gac acc tac				576
241	Ser Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala Cys Thr Asp Thr Tyr				
242	180	185		190	
243	ttt ata ggc ctc act gtt gtt ttc agt ggt gga gca ctc tgt atg gtc				624
244	Phe Ile Gly Leu Thr Val Val Phe Ser Gly Gly Ala Leu Cys Met Val				
245	195	200		205	
247	atc ttc acc ctt cta ata att tcc tat agg gtc atc cta aac tcc ctt				672
248	Ile Phe Thr Leu Leu Ile Ile Ser Tyr Arg Val Ile Leu Asn Ser Leu				
249	210	215		220	
251	aaa act tac act cag gaa ggg agg cat aaa gcc ctg tct acc tgc agc				720
252	Lys Thr Tyr Thr Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ser				
253	225	230		235	
255	tcc cac atc act gtg att gtt ctc ttt tta ttc cct gta ttt tca tat				768
256	Ser His Ile Thr Val Ile Val Leu Phe Leu Phe Pro Val Phe Ser Tyr				
257	240	245		250	
258	255				
259	gtg aga cct gtt tca aac ttt tct att gac aca ttc atg act gtc ttt				816
260	Val Arg Pro Val Ser Asn Phe Ser Ile Asp Thr Phe Met Thr Val Phe				
261	260	265		270	

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Input Set : A:\cura\_533\_us\_list.txt  
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263 tat aca gtt atc aca ccc aag ttg aat cct tta ata tac act ttc aga 864  
 264 Tyr Thr Val Ile Thr Pro Lys Leu Asn Pro Leu Ile Tyr Thr Phe Arg  
 265 275 280 285  
 267 aat tca gag atg aga aat gtt ata gaa aaa ctc ttg gtg aaa aag gta 912  
 268 Asn Ser Glu Met Arg Asn Val Ile Glu Lys Leu Leu Val Lys Lys Val  
 269 290 295 300  
 271 act ata ttt aga ata aca ggg tcc atc ctc atg tag 948  
 272 Thr Ile Phe Arg Ile Thr Gly Ser Ile Leu Met  
 273 305 310  
 275 <210> SEQ ID NO: 4  
 276 <211> LENGTH: 314  
 277 <212> TYPE: PRT  
 278 <213> ORGANISM: Homo sapiens  
 280 <400> SEQUENCE: 4  
 281 Met Arg Pro Asn Asn Ser Ile Thr Glu Phe Val Leu Leu Gly Phe Ser  
 282 1 5 10 15  
 284 Gln Asp Pro Gly Met Gln Lys Glu Leu Phe Val Met Phe Leu Phe Thr  
 285 20 25 30  
 287 Tyr Val Val Thr Val Leu Gly Asn Gln Leu Ile Val Val Thr Ile Ile  
 288 35 40 45  
 290 Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Cys Leu  
 291 50 55 60  
 293 Ser Phe Ile Asp Ala Ala Tyr Phe Thr Val Ile Ser Pro Lys Leu Ile  
 294 65 70 75 80  
 296 Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Gln Thr Phe Met  
 297 85 90 95  
 299 Gly Gln Leu Phe Ile Asp His Phe Phe Gly Gly Ala Glu Ala Phe Leu  
 300 100 105 110  
 302 Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Thr Leu  
 303 115 120 125  
 305 His Tyr Leu Thr Ile Met Thr Arg Gln Val Cys Ile Leu Ala Leu Leu  
 306 130 135 140  
 308 Val Ala Ala Thr Gly Gly Phe Val His Ser Val Phe Gln Ile Val Val  
 309 145 150 155 160  
 311 Val Tyr Ser Leu Pro Phe Cys Gly Ala Asn Val Ile Asp His Phe Ser  
 312 165 170 175  
 314 Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala Cys Thr Asp Thr Tyr Phe  
 315 180 185 190  
 317 Ile Gly Leu Thr Val Val Phe Ser Gly Gly Ala Leu Cys Met Val Ile  
 318 195 200 205  
 320 Phe Thr Leu Leu Ile Ile Ser Tyr Arg Val Ile Leu Asn Ser Leu Lys  
 321 210 215 220  
 323 Thr Tyr Thr Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser  
 324 225 230 235 240  
 326 His Ile Thr Val Ile Val Leu Phe Leu Phe Pro Val Phe Ser Tyr Val  
 327 245 250 255  
 329 Arg Pro Val Ser Asn Phe Ser Ile Asp Thr Phe Met Thr Val Phe Tyr  
 330 260 265 270  
 332 Thr Val Ile Thr Pro Lys Leu Asn Pro Leu Ile Tyr Thr Phe Arg Asn

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/04/2003  
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Input Set : A:\cura\_533\_us\_list.txt  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:51; Xaa Pos. 276  
Seq#:98; Xaa Pos. 286

**VERIFICATION SUMMARY**

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Input Set : A:\cura\_533\_us\_list.txt

Output Set: N:\CRF4\02042003\J041615.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:4011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:272

L:7241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:98 after pos.:272